Crosby\_9225-8866 (rev) available in PECAAN



Hitlist

Show  entries

| **Nr** | **Hit** | **Name** | **Probability** | **E-value** | **SS** | **Cols** | **Target Length** |
| --- | --- | --- | --- | --- | --- | --- | --- |
| 1 | [1MUL\_A](http://www.rcsb.org/pdb/explore/explore.do?structureId=1MUL) | DNA-binding protein HU-alpha; histone-like, DNA BINDING PROTEIN; 2.3A {Escherichia coli} SCOP: a.55.1.1 | 99.82 | 1.9e-21 | 13.6 | 90 | 90 |
| 2 | [d1mula\_](http://scop.berkeley.edu/sid%3Dd1mula_) | a.55.1.1 (A:) HU protein {Escherichia coli [TaxId: 562]} | 99.82 | 1.9e-21 | 13.6 | 90 | 90 |
| 3 | [1OWF\_A](http://www.rcsb.org/pdb/explore/explore.do?structureId=1OWF) | Integration Host Factor Alpha-subunit/Integration Host; protein-DNA recognition, indirect readout, IHF; 1.95A {Escherichia coli} SCOP: a.55.1.1 | 99.82 | 2.9e-21 | 14.4 | 99 | 99 |
| 4 | [PF00216.20](http://pfam.xfam.org/family/PF00216.20#tabview=tab0) | ; Bac\_DNA\_binding ; Bacterial DNA-binding protein | 99.82 | 2.3e-21 | 13.6 | 90 | 90 |
| 5 | [5FBM\_B](http://www.rcsb.org/pdb/explore/explore.do?structureId=5FBM) | DNA-binding protein HU; Histone-like protein, DNA binding, Dimerization; 1.9A {Streptococcus mutans serotype c (strain ATCC 700610 / UA159)} | 99.82 | 2.4e-21 | 13.8 | 91 | 99 |
| 6 | [d5lvta\_](http://scop.berkeley.edu/sid%3Dd5lvta_) | a.55.1.0 (A:) automated matches {Lactococcus lactis [TaxId: 272623]} | 99.81 | 3.8e-21 | 13.6 | 91 | 91 |
| 7 | [2NDP\_B](http://www.rcsb.org/pdb/explore/explore.do?structureId=2NDP) | Topoisomerase II subunit B (topIIB); Histone-like protein, DNA BINDING PROTEIN; NMR {Mycoplasma gallisepticum S6} | 99.81 | 6e-21 | 14.7 | 99 | 99 |
| 8 | [d2ndpa\_](http://scop.berkeley.edu/sid%3Dd2ndpa_) | a.55.1.0 (A:) automated matches {Mycoplasma gallisepticum [TaxId: 1006581]} | 99.81 | 6e-21 | 14.7 | 99 | 99 |
| 9 | [d1p71a\_](http://scop.berkeley.edu/sid%3Dd1p71a_) | a.55.1.1 (A:) HU protein {Anabaena sp. [TaxId: 1167]} | 99.81 | 4.2e-21 | 13.9 | 94 | 94 |
| 10 | [1P71\_A](http://www.rcsb.org/pdb/explore/explore.do?structureId=1P71) | DNA-BINDING PROTEIN HU/DNA Complex; protein-DNA complex, DNA bending, HU; 1.9A {Anabaena sp.} SCOP: a.55.1.1 | 99.81 | 4.2e-21 | 13.9 | 94 | 94 |
| 11 | [4P3V\_A](http://www.rcsb.org/pdb/explore/explore.do?structureId=4P3V) | DNA-binding protein HU-beta; Histone-like, homodimer, DNA BINDING PROTEIN; 1.25A {Escherichia coli} SCOP: a.55.1.1 | 99.8 | 6.9e-21 | 13.3 | 90 | 90 |
| 12 | [d4p3va\_](http://scop.berkeley.edu/sid%3Dd4p3va_) | a.55.1.1 (A:) HU protein {Escherichia coli, beta-isoform [TaxId: 562]} | 99.8 | 6.9e-21 | 13.3 | 90 | 90 |
| 13 | [d1owfa\_](http://scop.berkeley.edu/sid%3Dd1owfa_) | a.55.1.1 (A:) Integration host factor alpha subunit (IHFA) {Escherichia coli [TaxId: 562]} | 99.8 | 9.4e-21 | 13.9 | 94 | 96 |
| 14 | [2NP2\_B](http://www.rcsb.org/pdb/explore/explore.do?structureId=2NP2) | Hbb/DNA Complex; protein-dna complex, dna-binding protein, dna-bending; 3.02A {Borrelia burgdorferi} SCOP: a.55.1.0 | 99.8 | 1.2e-20 | 14.6 | 102 | 108 |
| 15 | [d1huua\_](http://scop.berkeley.edu/sid%3Dd1huua_) | a.55.1.1 (A:) HU protein {Bacillus stearothermophilus [TaxId: 1422]} | 99.79 | 1.3e-20 | 13.4 | 90 | 90 |
| 16 | [1HUU\_B](http://www.rcsb.org/pdb/explore/explore.do?structureId=1HUU) | PROTEIN HU; DNA-BINDING PROTEIN, DNA SUPERCOILING, ALPHA/BETA; 2.0A {Geobacillus stearothermophilus} SCOP: a.55.1.1 | 99.79 | 1.3e-20 | 13.4 | 90 | 90 |
| 17 | [1WTU\_A](http://www.rcsb.org/pdb/explore/explore.do?structureId=1WTU) | TRANSCRIPTION FACTOR 1; TRANSCRIPTION FACTOR, TYPE II DNA-BINDING; NMR {Bacillus phage SPO1} SCOP: a.55.1.1 | 99.79 | 1.5e-20 | 13.8 | 95 | 99 |
| 18 | [5EKA\_A](http://www.rcsb.org/pdb/explore/explore.do?structureId=5EKA) | DNA-binding protein HU; HU PROTEIN, HISTONE-LIKE PROTEIN, THERMOSTABLE; 1.69A {Thermus thermophilus HB8} | 99.79 | 1.8e-20 | 13.9 | 96 | 96 |
| 19 | [d5ekaa\_](http://scop.berkeley.edu/sid%3Dd5ekaa_) | a.55.1.0 (A:) automated matches {Thermus thermophilus [TaxId: 300852]} | 99.79 | 1.8e-20 | 13.9 | 96 | 96 |
| 20 | [d2np2a\_](http://scop.berkeley.edu/sid%3Dd2np2a_) | a.55.1.0 (A:) automated matches {Lyme disease spirochete (Borrelia burgdorferi) [TaxId: 139]} | 99.79 | 1.9e-20 | 14.2 | 96 | 102 |
| 21 | [d1owfb\_](http://scop.berkeley.edu/sid%3Dd1owfb_) | a.55.1.1 (B:) Integration host factor beta subunit (IHFB) {Escherichia coli [TaxId: 562]} | 99.79 | 1.7e-20 | 13.6 | 93 | 94 |
| 22 | [1OWF\_B](http://www.rcsb.org/pdb/explore/explore.do?structureId=1OWF) | Integration Host Factor Alpha-subunit/Integration Host; protein-DNA recognition, indirect readout, IHF; 1.95A {Escherichia coli} SCOP: a.55.1.1 | 99.79 | 1.7e-20 | 13.6 | 93 | 94 |
| 23 | [cd13835](http://www.ncbi.nlm.nih.gov/Structure/cdd/cddsrv.cgi?uid=cd13835) | IHF\_A; Alpha subunit of integration host factor (IHFA). This subfamily consists of the alpha subunit of integration host factor (IHF) and IHF-like domains. | 99.79 | 1.4e-20 | 13 | 88 | 88 |
| 24 | [cd13836](http://www.ncbi.nlm.nih.gov/Structure/cdd/cddsrv.cgi?uid=cd13836) | IHF\_B; Beta subunit of integration host factor (IHFB). This subfamily consists of the beta subunit of integration host factor (IHF) and IHF-like domains. | 99.79 | 1.1e-20 | 12.4 | 88 | 89 |
| 25 | [d3c4ia\_](http://scop.berkeley.edu/sid%3Dd3c4ia_) | a.55.1.0 (A:) automated matches {Mycobacterium tuberculosis [TaxId: 1773]} | 99.79 | 2.4e-20 | 14 | 98 | 99 |

Showing 1 to 25 of 250 entries

* Previous
* 1
* [2](https://toolkit.tuebingen.mpg.de/)
* [3](https://toolkit.tuebingen.mpg.de/)
* [4](https://toolkit.tuebingen.mpg.de/)
* [5](https://toolkit.tuebingen.mpg.de/)
* …
* [10](https://toolkit.tuebingen.mpg.de/)
* [Next](https://toolkit.tuebingen.mpg.de/)

Alignments

Top of Form

|  |  |  |
| --- | --- | --- |
|  | Template alignment | Template 3D structure | [PDBe](http://www.ebi.ac.uk/pdbe/entry/pdb/1mul%22%20%5Ct%20%22_blank) |  |
| **1.** | [**1MUL\_A**](http://www.rcsb.org/pdb/explore/explore.do?structureId=1MUL)**DNA-binding protein HU-alpha; histone-like, DNA BINDING PROTEIN; 2.3A {Escherichia coli} SCOP: a.55.1.1; Related PDB entries: 4YEY\_A 4YEY\_C 4YF0\_A 4YF0\_B 2O97\_A 4YEW\_C 4YEX\_A 4YEX\_C 4YFT\_C 4YFH\_A 4YFH\_B** |
|  | Probability: 99.82   E-value: 1.9E-21   Score: 119.69   Aligned Cols: 90   Identities: 24%   Similarity: 0.375   |
|  |  |  |  |  |
|  | Q ss\_pred |  | CCHHHHHHHHHHHhCCCHHHHHHHHHHHHHHHHHHHhCCCcEEeCCCeEEEEEEeCCceeECCCCCCeEE |  |
|  | Q Q\_5758367 | 11 | LSRTSLGEAVALQMGVSLEQGHEAVFAVLEVITKTLAGGYGVTVTNFGSWHPVVAPARRAHNPQTMEPVQ 80 (119) |  |
|  | Q Consensus  | 11 | ~t~~el~~~ia~~~~~~~~~v~~v~~~l~~~i~~~L~~G~~V~l~glG~f~~~~~~~~~~~~p~~~~~~~ 80 (119) |  |
|  |  |  | |+.++|++.||+++++++.++..+++.+.+.|.++|.+|++|.|.|||+|++...+.+...+|.+++... |  |
|  | T Consensus  | 1 | m~~~~l~~~ia~~~~~~~~~v~~v~~~~~~~i~~~L~~g~~V~l~g~G~f~~~~~~~~~~~~~~~~~~~~ 70 (90) |  |
|  | T 1MUL\_A | 1 | MNKTQLIDVIAEKAELSKTQAKAALESTLAAITESLKEGDAVQLVGFGTFKVNHRAERTGRNPQTGKEIK 70 (90) |  |
|  | T ss\_dssp |  | CCHHHHHHHHHHHTTCCHHHHHHHHHHHHHHHHHHHHTTCCEEETTTEEEEEEEECC------------- |  |
|  | T ss\_pred |  | CCHHHHHHHHHHHHCCCHHHHHHHHHHHHHHHHHHHHcCCcEEeCCCeEEEEEEeCCeeEeCCCCCCEEE |  |
|  |  |  |
|  |  |  |
|  | Q ss\_pred |  | eCCcceeEEEeCHHHHHHHc |  |
|  | Q Q\_5758367 | 81 | VAESFKVKWTTSPKLREIVN 100 (119) |  |
|  | Q Consensus  | 81 | ~~~~~~v~F~p~~~lk~~l~ 100 (119) |  |
|  |  |  | ++++..|+|+|++.|++.|+ |  |
|  | T Consensus  | 71 | ~~~~~~v~f~p~~~lk~~l~ 90 (90) |  |
|  | T 1MUL\_A | 71 | IAAANVPAFVSGKALKDAVK 90 (90) |  |
|  | T ss\_dssp |  | -CCEEEEEEEECHHHHHHHC |  |
|  | T ss\_pred |  | eCCeeeeEEEeCHHHHHHhC |  |
|  |  |  |
|  |  |  |
|  |
|  | Template alignment | Template 3D structure | [PDB](http://www.rcsb.org/pdb/explore/explore.do?structureId=1mul) | [NCBI](http://www.ncbi.nlm.nih.gov/entrez/query.fcgi?SUBMIT=y&db=structure&orig_db=structure&term=1mul) |  |
| **2.** | [**d1mula\_**](http://scop.berkeley.edu/sid%3Dd1mula_)**a.55.1.1 (A:) HU protein {Escherichia coli [TaxId: 562]}** |
|  | Probability: 99.82   E-value: 1.9E-21   Score: 119.69   Aligned Cols: 90   Identities: 24%   Similarity: 0.375   |
|  |  |  |  |  |
|  | Q ss\_pred |  | CCHHHHHHHHHHHhCCCHHHHHHHHHHHHHHHHHHHhCCCcEEeCCCeEEEEEEeCCceeECCCCCCeEE |  |
|  | Q Q\_5758367 | 11 | LSRTSLGEAVALQMGVSLEQGHEAVFAVLEVITKTLAGGYGVTVTNFGSWHPVVAPARRAHNPQTMEPVQ 80 (119) |  |
|  | Q Consensus  | 11 | ~t~~el~~~ia~~~~~~~~~v~~v~~~l~~~i~~~L~~G~~V~l~glG~f~~~~~~~~~~~~p~~~~~~~ 80 (119) |  |
|  |  |  | |+.++|++.||+++++++.++..+++.+.+.|.++|.+|++|.|.|||+|++...+.+...+|.+++... |  |
|  | T Consensus  | 1 | m~~~~l~~~ia~~~~~~~~~v~~v~~~~~~~i~~~L~~g~~V~l~g~G~f~~~~~~~~~~~~~~~~~~~~ 70 (90) |  |
|  | T d1mula\_ | 1 | MNKTQLIDVIAEKAELSKTQAKAALESTLAAITESLKEGDAVQLVGFGTFKVNHRAERTGRNPQTGKEIK 70 (90) |  |
|  | T ss\_dssp |  | CCHHHHHHHHHHHTTCCHHHHHHHHHHHHHHHHHHHHTTCCEEETTTEEEEEEEECC------------- |  |
|  | T ss\_pred |  | CCHHHHHHHHHHHHCCCHHHHHHHHHHHHHHHHHHHHcCCcEEeCCCeEEEEEEeCCeeEeCCCCCCEEE |  |
|  |  |  |
|  |  |  |
|  | Q ss\_pred |  | eCCcceeEEEeCHHHHHHHc |  |
|  | Q Q\_5758367 | 81 | VAESFKVKWTTSPKLREIVN 100 (119) |  |
|  | Q Consensus  | 81 | ~~~~~~v~F~p~~~lk~~l~ 100 (119) |  |
|  |  |  | ++++..|+|+|++.|++.|+ |  |
|  | T Consensus  | 71 | ~~~~~~v~f~p~~~lk~~l~ 90 (90) |  |
|  | T d1mula\_ | 71 | IAAANVPAFVSGKALKDAVK 90 (90) |  |
|  | T ss\_dssp |  | -CCEEEEEEEECHHHHHHHC |  |
|  | T ss\_pred |  | eCCeeeeEEEeCHHHHHHhC |  |
|  |  |  |
|  |  |  |
|  |
|  | Template alignment | Template 3D structure | [PDBe](http://www.ebi.ac.uk/pdbe/entry/pdb/1owf%22%20%5Ct%20%22_blank) |  |
| **3.** | [**1OWF\_A**](http://www.rcsb.org/pdb/explore/explore.do?structureId=1OWF)**Integration Host Factor Alpha-subunit/Integration Host; protein-DNA recognition, indirect readout, IHF; 1.95A {Escherichia coli} SCOP: a.55.1.1; Related PDB entries: 2HT0\_A 1IHF\_A 1OUZ\_A 1OWG\_A 5WFE\_K 5J0N\_K 5J0N\_I** |
|  | Probability: 99.82   E-value: 2.9E-21   Score: 120.96   Aligned Cols: 99   Identities: 22%   Similarity: 0.33   |
|  |  |  |  |  |
|  | Q ss\_pred |  | CCCCHHHHHHHHHHHhCCCHHHHHHHHHHHHHHHHHHHhCCCcEEeCCCeEEEEEEeCCceeECCCCCCe |  |
|  | Q Q\_5758367 | 9 | HDLSRTSLGEAVALQMGVSLEQGHEAVFAVLEVITKTLAGGYGVTVTNFGSWHPVVAPARRAHNPQTMEP 78 (119) |  |
|  | Q Consensus  | 9 | ~~~t~~el~~~ia~~~~~~~~~v~~v~~~l~~~i~~~L~~G~~V~l~glG~f~~~~~~~~~~~~p~~~~~ 78 (119) |  |
|  |  |  | ++|+.++|++.|++++++++.++..+++.+.+.|.++|.+|++|.|.|||+|++...+.+...+|.+|+. |  |
|  | T Consensus  | 1 | ~~~~~~~l~~~ia~~~~~s~~~v~~~l~~~~~~i~~~L~~g~~V~l~g~G~f~~~~~~~~~~~~~~~~~~ 70 (99) |  |
|  | T 1OWF\_A | 1 | MALTKAEMSEYLFDKLGLSKRDAKELVELFFEEIRRALENGEQVKLSGFGNFDLRDKNQRPGRNPKTGED 70 (99) |  |
|  | T ss\_dssp |  | -CBCHHHHHHHHHHHHCCCHHHHHHHHHHHHHHHHHHHHTTCCEEETTTEEEEEEEECCEEEECSSSCCE |  |
|  | T ss\_pred |  | CCcCHHHHHHHHHHHHCCCHHHHHHHHHHHHHHHHHHHHCCCcEEcCCCeEEEEEEeCCCeeeCCCCCCE |  |
|  |  |  |
|  |  |  |
|  | Q ss\_pred |  | EEeCCcceeEEEeCHHHHHHHcccccccc |  |
|  | Q Q\_5758367 | 79 | VQVAESFKVKWTTSPKLREIVNGEAAPTI 107 (119) |  |
|  | Q Consensus  | 79 | ~~~~~~~~v~F~p~~~lk~~l~~~~~~~~ 107 (119) |  |
|  |  |  | ..++++..|+|+|++.|+++++....... |  |
|  | T Consensus  | 71 | ~~i~~~~~v~F~p~~~lk~~l~~~~~~~~ 99 (99) |  |
|  | T 1OWF\_A | 71 | IPITARRVVTFRPGQKLKSRVENASPKDE 99 (99) |  |
|  | T ss\_dssp |  | EEECCEEEEEEEECHHHHHHHHTCCCC-- |  |
|  | T ss\_pred |  | EEeCCceeEEEEeCHHHHHHHhccCCCCC |  |
|  |  |  |
|  |  |  |
|  |
|  | Template alignment | [CDD](http://www.ncbi.nlm.nih.gov/Structure/cdd/cddsrv.cgi?uid=pfam00216) |  |
| **4.** | [**PF00216.20**](http://pfam.xfam.org/family/PF00216.20#tabview=tab0)**; Bac\_DNA\_binding ; Bacterial DNA-binding protein** |
|  | Probability: 99.82   E-value: 2.3E-21   Score: 119.36   Aligned Cols: 90   Identities: 21%   Similarity: 0.435   |
|  |  |  |  |  |
|  | Q ss\_pred |  | CCHHHHHHHHHHHhCCCHHHHHHHHHHHHHHHHHHHhCCCcEEeCCCeEEEEEEeCCceeECCCCCCeEE |  |
|  | Q Q\_5758367 | 11 | LSRTSLGEAVALQMGVSLEQGHEAVFAVLEVITKTLAGGYGVTVTNFGSWHPVVAPARRAHNPQTMEPVQ 80 (119) |  |
|  | Q Consensus  | 11 | ~t~~el~~~ia~~~~~~~~~v~~v~~~l~~~i~~~L~~G~~V~l~glG~f~~~~~~~~~~~~p~~~~~~~ 80 (119) |  |
|  |  |  | |+.++|+++|++.++++++++..+++.+.+.|.++|.+|++|.|.|||+|++...+.+..+||.+++.+. |  |
|  | T Consensus  | 1 | m~~~~l~~~ia~~~~~~~~~~~~~~~~~~~~i~~~L~~G~~V~l~g~G~f~~~~~~~~~~~~~~~~~~~~ 70 (90) |  |
|  | T PF00216.20 | 1 | MNSNDLVDRIASGQGLTKTDAKKLVDAVFSTIVDAAVAGEEIALNGFGKFKVKHSAARKGHNPATLQEIE 70 (90) |  |
|  | T ss\_pred |  | CCHHHHHHHHHHhhCCCHHHHHHHHHHHHHHHHHHHHcCCeEEeCCCEEEEEEEeCCceeeCCCCCCEEE |  |
|  |  |  |
|  |  |  |
|  | Q ss\_pred |  | eCCcceeEEEeCHHHHHHHc |  |
|  | Q Q\_5758367 | 81 | VAESFKVKWTTSPKLREIVN 100 (119) |  |
|  | Q Consensus  | 81 | ~~~~~~v~F~p~~~lk~~l~ 100 (119) |  |
|  |  |  | ++++..++|+|++.|+++++ |  |
|  | T Consensus  | 71 | v~~~~~v~F~~~~~lk~~l~ 90 (90) |  |
|  | T PF00216.20 | 71 | IPASNRLTFTSAKAVKDRLN 90 (90) |  |
|  | T ss\_pred |  | eCCcceEEEEeCHHHHHHhC |  |
|  |  |  |
|  |  |  |
|  |
|  | Template alignment | Template 3D structure | [PDBe](http://www.ebi.ac.uk/pdbe/entry/pdb/5fbm%22%20%5Ct%20%22_blank) |  |
| **5.** | [**5FBM\_B**](http://www.rcsb.org/pdb/explore/explore.do?structureId=5FBM)**DNA-binding protein HU; Histone-like protein, DNA binding, Dimerization; 1.9A {Streptococcus mutans serotype c (strain ATCC 700610 / UA159)}; Related PDB entries: 5FBM\_A 4QJN\_A 4QJN\_D 4QJN\_B 4QJN\_C 4QJU\_A 4QJU\_B 5LVT\_A 5LVT\_D 5LVT\_B 5LVT\_C** |
|  | Probability: 99.82   E-value: 2.4E-21   Score: 121.98   Aligned Cols: 91   Identities: 25%   Similarity: 0.32   |
|  |  |  |  |  |
|  | Q ss\_pred |  | CCCHHHHHHHHHHHhCCCHHHHHHHHHHHHHHHHHHHhCCCcEEeCCCeEEEEEEeCCceeECCCCCCeE |  |
|  | Q Q\_5758367 | 10 | DLSRTSLGEAVALQMGVSLEQGHEAVFAVLEVITKTLAGGYGVTVTNFGSWHPVVAPARRAHNPQTMEPV 79 (119) |  |
|  | Q Consensus  | 10 | ~~t~~el~~~ia~~~~~~~~~v~~v~~~l~~~i~~~L~~G~~V~l~glG~f~~~~~~~~~~~~p~~~~~~ 79 (119) |  |
|  |  |  | .|+.++|++.||++++++++++..+++.+.+.|.++|.+|++|.|.|||+|++...+.+...||.+|+.+ |  |
|  | T Consensus  | 1 | ~m~~~~li~~ia~~~~is~~~v~~vl~~l~~~i~e~L~~g~~V~l~g~G~f~~~~~~~~~~~~p~t~~~~ 70 (99) |  |
|  | T 5FBM\_B | 1 | MANKQDLIAKVAEATELTKKDSAAAVDAVFSAVSSYLAKGEKVQLIGFGNFEVRERAARKGRNPQTGEEI 70 (99) |  |
|  | T ss\_dssp |  | -CBHHHHHHHHHHHSSCCHHHHHHHHHHHHHHHHHHHHTTCCEEETTTEEEEEEEECCBC-------CCC |  |
|  | T ss\_pred |  | CCCHHHHHHHHHHHhCCCHHHHHHHHHHHHHHHHHHHHcCCcEEcCCCeEEEEEEeCCceEECCCCCCEE |  |
|  |  |  |
|  |  |  |
|  | Q ss\_pred |  | EeCCcceeEEEeCHHHHHHHc |  |
|  | Q Q\_5758367 | 80 | QVAESFKVKWTTSPKLREIVN 100 (119) |  |
|  | Q Consensus  | 80 | ~~~~~~~v~F~p~~~lk~~l~ 100 (119) |  |
|  |  |  | .++++..|+|+|++.|++.+. |  |
|  | T Consensus  | 71 | ~i~~~~~i~F~psk~lk~~~~ 91 (99) |  |
|  | T 5FBM\_B | 71 | KIKASKVPAFKAGKALKDAVK 91 (99) |  |
|  | T ss\_dssp |  | CBCCEEEEEEEECHHHHHHHC |  |
|  | T ss\_pred |  | EeCCeeeeEEEeCHHHHHHHh |  |
|  |  |  |
|  |  |  |